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Set	Items	Description
S1	5934	RELAXIN
S2	1251093	RECOMBINANT? OR CDNA OR VECTOR OR COLI
S3	327	S1 AND S2
S4	192	RD (unique items)
S5	158	PREPRORELAXIN OR PRORELAXIN
S6	18	S5 AND S2 NOT S3

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Rev 1/94
PBT

STRUCTURE FILE UPDATES: 15 APR 94 HIGHEST RN 154427-83-5
DICTIONARY FILE UPDATES: 18 APR 94 HIGHEST RN 154427-83-5

TSCA INFORMATION NOW CURRENT THROUGH 30 JUNE 1993

=> e krkptgygsrkk/r/sqep

E1	1	KRKH/SQEP
E2	1	KRKPDVGGFMVEDQRTHKSHNYMMKRARNDVLGDKENVRPNPYYTEPFDPDTSP EELSALIVDYANMIRNDVILLDNSVERTRTRKRGNIQVENQAIPDPPCTCKYKKE IEDLGENSVPRFIELTRNCNKTQQPTCRPPYICKESLYSITILKRRETKSQESLE IPNELKYRWVAESHPVSVACLLCTRDYQLRYNNN/SQEP
E3	0 -->	KRKPTGYGSRKKR/SQEP
E4	1	KRKQGSVRGL/SQEP
E5	1	KRKQISGRGL/SQEP
E6	1	KRKQISVAGL/SQEP
E7	1	KRKQISVGGL/SQEP
E8	1	KRKQISVSR/SQEP
E9	1	KRKQISVRG/SQEP
E10	1	KRKQISVRGL/SQEP
E11	2	KRK/SQEP
E12	1	KRKRGGGKRKR/SQEP

=> s krkptgygsrkk/r/sqsp

L1 0 KRKPTGYGSRKKR/SQSP

=> e dkkrtgygsrrrk/sqep

E1	1	DKKQRFHNIR/SQEP
E2	1	DKKR/SQEP
E3	0 -->	DKKRTGYGSRRRK/SQEP
E4	1	DKKSPKKAK'ORN'GRR/SQEP
E5	1	DKKTEETTHLEDRLITTRHNTTSTTQSSVGVTYGYASADRFLPGPNNTSGLESR VEQAERFFKEKLFTWTASQEFAHVHLELPTDHKGIVGAMVESAYVRNGWDVQ VSATSTQFNNGTLLVAMVPELSHLDKRDVSQTLTFPHQYINPRTNTTAHIVVPY VGVRNRHDQVQMHKAWTLVVEVMAPLTTSNMGQDNVEVY/SQEP
E6	1	DKKTEETTLEDRILTTTRNGHTTQSSVGVTYGYSTQEDHVSQPNNTSGLETR VVQAERFFKKHLFDWTPDKAFGHLEKELPTDHKGIVGHLVDSFAYMRNGWDVE VSAVGNQFNNGCLLVAMVPEWKEFTPKEFYQLTLFPHQFISPRTNMTAHIVVPY LGVNRYDQYKKHKPWTLVVMVSPLTNTVSAGQIKVY/SQEP
E7	1	DKKTEETTLEDRILTTTRNGHTTSTTQSSVGVTYGYATAEDFVSGPNNTSGLETR VVQAERFFKTHLFDWVTSDFGRCHLLELPTDHKGIVGSLTDYAYMRNGWDVE VTAVGNQFNNGCLLVAMVPELCSIQKRELYQLTLFPHQFINPRTNMTAHITVPF VGVNRYDQYKVHKPWTLVVMVAPLTNVNEGAPQIKVY/SQEP
E8	1	DKKTEETTLEDRILTTTRNGHTTSTTQSSVGVTYGYATAEDFVSGPNNTSGLETR VVQAERFFKTHLFDWVTSDFGRCHLLELPTDHKGIVGSLTDYAYMRNGWDVE VTAVGNQFNNGCLLVAMVPELYSIQKRELYQLTLFPHQFINPRTNMTAHITVPF VGVNRYDQYKVHKPWTLVVMVAPLTNVNEGAPQIKVY/SQEP
E9	1	DKKTEETTLEDRILTTTRNGHTTSTTQSSVGVTYGYSTEEDHVAGPNNTSGLETR VVQAERFFKKFLFDWTPDKFGHRTKLELPTDHGVFGHLVDSYAYMRNGWDVE VSAVGNQFNNGCLLVAMVPEWKFDTREYQLTLFPHQFISPRTNMTAHITVPF LGVNRYDQYKKHKPWTLVIMVLSPLTVSNTAATQIKVY/SQEP
E10	1	DKKTEETTLEDRILTTTRNGHTTSTTQSSVGVTYGYSTEEDHVAGPNNTSGLETR VVQAERFFKKFLFDWTTDKPFGYLTKELPTDHGVFGHLVDSYAYMRNGWDVE VCAVGNQFNNGCLLVAMVPEWKFDTREYQLTLFPHQFISPRTNMTAHITVPF LGVNRYDQYKKHKPWTLVVMVLSPLTVSNTAAPQIKVY/SQEP
E11	1	DKKTEETTLEDRILTTTRNGHTTSTTQSSVGVTYGYSTEEDHVAGPNNTSGLETR VVQAERFFKKFLFDWTTDKPFGYLTKELPTDHGVFGHLVDSYAYMRNGWDVE VSAVGNQFNNGCLLVAMVPEWKFDTREYQLTLFPHQFISPRTNMTAHITVPF

E12

1

I [REDACTED] NRYDQYKKHKPWTLVVMVLSPLTVS [REDACTED] AAPQIKVY / SQEP
DKKTEETTLEDRILTTTRNGQTTSTTQS [REDACTED] GVTLGYATAEDSTSGPNTSGLETR
VHQAEFFKMFALFDWVPSQNFGHMHKVVLPHEPKGVYGLVKSYAYMRNGWDVE
VTAVGNQFNGGCLQAALVPEMGIISDREKYQLTLYPHQFINPRTNMTAHTIVPY
GGVNRYDQYKQHRPWTLVMMVAPLTNTAGAQQIKVY / SQEP

=> s dkkrtgygsrrrk/sqsp

L2 0 DKKRTGYGSRRRK/SQSP

=> s dkkrtgygsrkr/sqsp

L3 0 DKKRTGYGSRKKR/SQSP

=> e dkkrtgygsrkr/sqep

E1 1 DKKQRFHNIR/SQEP

E2 1 DKKR/SQEP

E3 0 --> DKKRTGYGSRKKR/SQEP

E4 1 DKKSPKKAK'ORN'GRR/SQEP

E5 1 DKKTEETTHLEDRLITTRHNTTSTTQSSVGVTYGYASADRFLPGPNTSGLESR
VEQAERFFKEKLFTWTASQEFAHVHLELPTDHKGIVGAMVESHAVRNGWDVQ
VSATSTQFNGGTLLVAMVPELSHLDKRDVSQQLTLFPHQYINPRTNTTAHIVVPY
VGVNRHQDVQVQMHKAWTLVVEVMAPLTTSNMGQDNVEVY / SQEP

E6 1 DKKTEETTLEDRILTTTRNGHTTQSSVGVTYGYSTQEDHVSGPNTSGLETR
VVQAERFFKKHLFDWTPDKAFGHLEKLELPTDHKGIVGHLVDSFAYMRNGWDV
VSAVGNQFNGGCLLVAMVPEWKEFTPREEYQLTLFPHQFISPRTNMTAHTIVVPY
LGVNRYDQYKKHKPWTLVMMVSPLTNTVSAGQIKVY / SQEP

E7 1 DKKTEETTLEDRILTTTRNGHTTSTTQSSVGVTYGYATAEDFVSGPNTSGLETR
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VGVNRYDQYKVKHPWTLVMMVAPLTVNNEGAPQIKVY / SQEP

E8 1 DKKTEETTLEDRILTTTRNGHTTSTTQSSVGVTYGYATAEDFVSGPNTSGLETR
VVQAERFFKKTHLFDWVTSDPFGRCHELLELPTDHKGIVGSLTDSYAYMRNGWDV
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VGVNRYDQYKVKHPWTLVMMVAPLTVNTEGAPQIKVY / SQEP

E9 1 DKKTEETTLEDRILTTTRNGHTTSTTQSSVGVTYGYSTEEDHVAGPNTSGLETR
VVQAERFFKKFLFDWTPDKFGHRTKELLELPTDHKGIVGHLVDSYAYMRNGWDV
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LGVNRYDQYKKHKPWTLVIMVLSPLTVSNTAATQIKVY / SQEP

E10 1 DKKTEETTLEDRILTTTRNGHTTSTTQSSVGVTYGYSTEEDHVAGPNTSGLETR
VVQAERFFKKFLFDWTTDKPFGYLTKELELPTDHKGIVGHLVDSYAYMRNGWDV
VCAVGNQFNGGCLLVAMVPEWKAFTDTREKYQLTLFPHQFITPRTNMTAHTIVPY
LGVNRYDQYKKHKPWTLVMMVLSPLTVSNTAAPQIKVY / SQEP

E11 1 DKKTEETTLEDRILTTTRNGHTTSTTQSSVGVTYGYSTEEDHVAGPNTSGLETR
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VSAVGNQFNGGCLLVAMVPEWKAFTDTREKYQLTLFPHQFISPRTNMTAHTIVPY
LGVNRYDQYKKHKPWTLVMMVLSPLTVSNTAAPQIKVY / SQEP

E12 1 DKKTEETTLEDRILTTTRNGQTTSTTQSSVGVTLGYATAEDSTSGPNTSGLETR
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VTAVGNQFNGGCLQAALVPEMGIISDREKYQLTLYPHQFINPRTNMTAHTIVPY
GGVNRYDQYKQHRPWTLVMMVAPLTNTAGAQQIKVY / SQEP

=> e krkptgygsrrrk/sqsp

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=> s krkptgygsrrrk/sqsp

L4 0 KRKPTGYGSRRRK/SQSP

=> e krkptgygsrrrk/sqep

E1	1	I H/SQEP
E2	1	K KPDVGGFMVEDQRTHKSHNYMMKRAR..JVLGDKENVRPNPYYTEPFDPDTSP EELSALIVDYANMIRNDVILLDNSVETRTRKRGNIQVENQAIPDPPCTCKYKKE IEDLGENSVPRFIETRNCNKTQQPTCRPPYICKESLYSITILKRRETKSQESLE IPNELKYRWVAESHPVSVACLCTRDYQLRYNNN/SQEP
E3	0 -->	KRKPTGYGSRRRK/SQEP
E4	1	KRKQGSVRGL/SQEP
E5	1	KRKQISGRGL/SQEP
E6	1	KRKQISVAGL/SQEP
E7	1	KRKQISVGGL/SQEP
E8	1	KRKQISVR/SQEP
E9	1	KRKQISVRG/SQEP
E10	1	KRKQISVRGL/SQEP
E11	2	KRKR/SQEP
E12	1	KRKRGGGKRKR/SQEP